

Appendix B

NCBI Entrez BLAST 2 sequences BLAST 2 sequences Example Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#).

Reference: Tatjana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

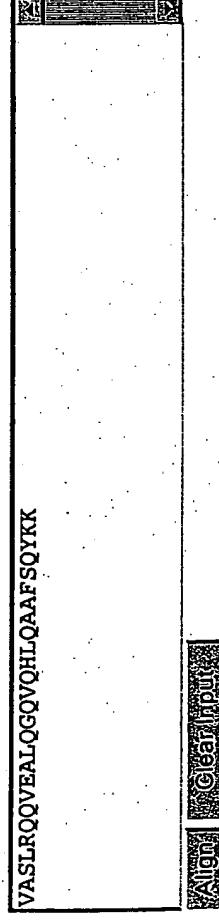
Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

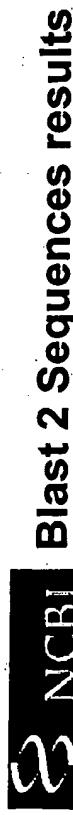
Use Mega BLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

<input type="button



Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

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[Entrez](#)

[BLAST](#)

[OMIM](#)

[Taxonomy](#)

[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

A 3/3

NCBI Entrez BLAST BLAST 2 sequences Example Help

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Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

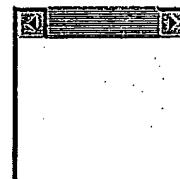
Reward for a match: Penalty for a mismatch:

Use MegaBLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

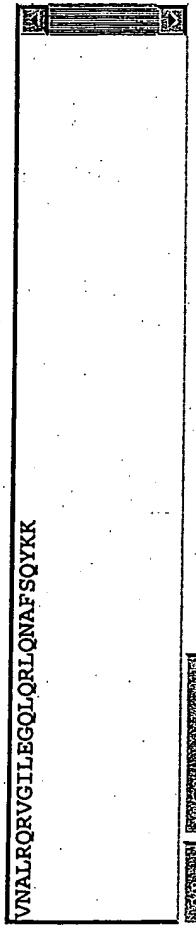
Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

LXXXXXXEVXXLKEKQALQTVCVCL


Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

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Comments and suggestions to blast-help@ncbi.nlm.nih.gov

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NCBI Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

B 3/3

NCBI

Entrez

BLAST

BLAST 2 sequences

Help

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Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use MegabLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file

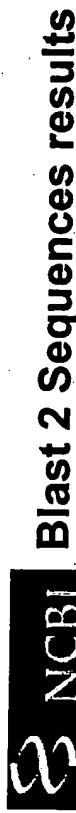
or sequence in FASTA format from: to:

LXXXXXXEVEVXXLREXQALQTVCL

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

SAAIRQQMEALLNGKLQRLEAFSRYKK
<input type="checkbox"/> Align <input checked="" type="checkbox"/> Clear All

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Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

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C 3/3

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Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to:

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

D 1/3

VNALKQRVTILDGHLRRFQNAFSQYKK

VNALKQRVTILDGHLLRRFONAFAQSQYKK

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

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D2/3



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix [BLOSUM62](#) gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

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BLAST 2 SEQUENCES

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Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

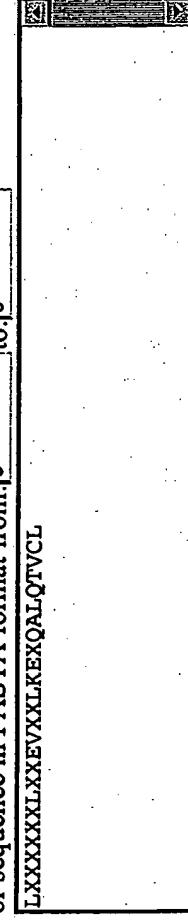
Reward for a match: Penalty for a mismatch:

Use MegaBLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

XXXXXXXXXXXXXXLREXQALQTVCCL


Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

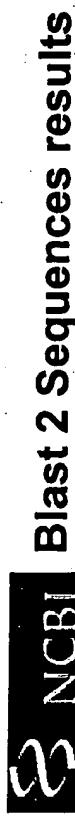
VDTLRORMRNLEGEVORLONIVTQYRK	
<input type="button" value="Align"/>	<input type="button" value="Create Input"/>

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

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Blast 2 Sequences results

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E 3/3